

10/554561

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SEQUENCE LISTING

<110> YOUSUKE, EBINA
TOSHIYUKI, OBATA
MEDICAL AND BIOLOGICAL LABORATORIES CO., LTD.

<120> METHOD FOR DETERMINATION OF INSULIN RECEPTOR ALPHA SUBUNIT

<130> M3-A0301Y1P

<150> JP 2003-121955

<151> 2003-04-25

<150> JP 2003-433303

<151> 2003-12-26

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<170> PatentIn version 3.1

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 Leu Ile Met Ile Thr Asp Tyr Leu Leu Leu Phe Arg Val Tyr Gly Leu
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 Arg Leu Phe Phe Asn Tyr Ala Leu Val Ile Phe Glu Met Val His Leu
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855 860 865

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10/554561

SEQUENCE LISTING

<110> Ebina, Yousuke
Obata, Toshiyuki
Okamoto, Eiji

JC20 Rec'd PCT/PTO 25 OCT 2005

<120> METHODS FOR MEASURING THE INSULIN
RECEPTOR ALPHA SUBUNIT

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<150> PCT/JP2004/005412
<151> 2004-04-15

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Val Ile His Asn Asn Lys Cys Ile Pro Glu Cys Pro Ser Gly Tyr Thr	
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aga aac gac att gcc ctg aag acc aat ggg gac aag gca tcc tgt gaa			1488
Arg Asn Asp Ile Ala Leu Lys Thr Asn Gly Asp Lys Ala Ser Cys Glu			
455	460	465	
aat gag tta ctt aaa ttt tct tac att cgg aca tct ttt gac aag atc			1536
Asn Glu Leu Leu Lys Phe Ser Tyr Ile Arg Thr Ser Phe Asp Lys Ile			
470	475	480	485
ttg ctg aga tgg gag ccg tac tgg ccc ccc gac ttc cga gac ctc ttg			1584
Leu Leu Arg Trp Glu Pro Tyr Trp Pro Pro Asp Phe Arg Asp Leu Leu			
490	495	500	
ggg ttc atg ctg ttc tac aaa gag gcc cct tat cag aat gtg acg gag			1632
Gly Phe Met Leu Phe Tyr Lys Glu Ala Pro Tyr Gln Asn Val Thr Glu			
505	510	515	
ttc gat ggg cag gat gcg tgt ggt tcc aac agt tgg acg gtg gta gac			1680
Phe Asp Gly Gln Asp Ala Cys Gly Ser Asn Ser Trp Thr Val Val Asp			
520	525	530	
att gac cca ccc ctg agg tcc aac gac ccc aaa tca cag aac cac cca			1728
Ile Asp Pro Pro Leu Arg Ser Asn Asp Pro Lys Ser Gln Asn His Pro			

535	540	545	
ggg tgg ctg atg cgg ggt ctc aag ccc tgg acc cag tat gcc atc ttt Gly Trp Leu Met Arg Gly Leu Lys Pro Trp Thr Gln Tyr Ala Ile Phe 550 555 560 565			1776
gtg aag acc ctg gtc acc ttt tcg gat gaa cgc cgg acc tat ggg gcc Val Lys Thr Leu Val Thr Phe Ser Asp Glu Arg Arg Thr Tyr Gly Ala 570 575 580			1824
aag agt gac atc att tat gtc cag aca gat gcc acc aac ccc tct gtg Lys Ser Asp Ile Ile Tyr Val Gln Thr Asp Ala Thr Asn Pro Ser Val 585 590 595			1872
ccc ctg gat cca atc tca gtg tct aac tca tca tcc cag att att ctg Pro Leu Asp Pro Ile Ser Val Ser Asn Ser Ser Gln Ile Ile Leu 600 605 610			1920
aag tgg aaa cca ccc tcc gac ccc aat ggc aac atc acc cac tac ctg Lys Trp Lys Pro Pro Ser Asp Pro Asn Gly Asn Ile Thr His Tyr Leu 615 620 625			1968
gtt ttc tgg gag agg cag gcg gaa gac agt gag ctg ttc gag ctg gat Val Phe Trp Glu Arg Gln Ala Glu Asp Ser Glu Leu Phe Glu Leu Asp 630 635 640 645			2016
tat tgc ctc aaa ggg ctg aag ctg ccc tcg agg acc tgg tct cca cca Tyr Cys Leu Lys Gly Leu Lys Leu Pro Ser Arg Thr Trp Ser Pro Pro 650 655 660			2064
ttc gag tct gaa gat tct cag aag cac aac cag agt gag tat gag gat Phe Glu Ser Glu Asp Ser Gln Lys His Asn Gln Ser Glu Tyr Glu Asp 665 670 675			2112
tcg gcc ggc gaa tgc tgc tcc tgt cca aag aca gac tct cag atc ctg Ser Ala Gly Glu Cys Cys Ser Cys Pro Lys Thr Asp Ser Gln Ile Leu 680 685 690			2160
aag gag ctg gag gag tcc tcg ttt agg aag acg ttt gag gat tac ctg Lys Glu Leu Glu Ser Ser Phe Arg Lys Thr Phe Glu Asp Tyr Leu 695 700 705			2208
cac aac gtg gtt ttc gtc ccc aga aaa acc tct tca ggc act ggt gcc His Asn Val Val Phe Val Pro Arg Lys Thr Ser Ser Gly Thr Gly Ala 710 715 720 725			2256
gag gac cct agg cca tct cgg aaa cgc agg tcc ctt ggc gat gtt ggg Glu Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly 730 735 740			2304
aat gtg acg gtg gcc gtg ccc acg gtg gca gct ttc ccc aac act tcc Asn Val Thr Val Ala Val Pro Thr Val Ala Ala Phe Pro Asn Thr Ser 745 750 755			2352
tcg acc agc gtg ccc acg agt ccg gag gag cac agg cct ttt gag aag Ser Thr Ser Val Pro Thr Ser Pro Glu Glu His Arg Pro Phe Glu Lys 760 765 770			2400
gtg gtg aac aag gag tcg ctg gtc atc tcc ggc ttg cga cac ttc acg Val Val Asn Lys Glu Ser Leu Val Ile Ser Gly Leu Arg His Phe Thr			2448

775	780	785	
ggc tat cgc atc gag ctg cag gct tgc aac cag gac acc cct gag gaa Gly Tyr Arg Ile Glu Leu Gln Ala Cys Asn Gln Asp Thr Pro Glu Glu 790 795 800 805			2496
cgg tgc agt gtg gca gcc tac gtc agt gcg agg acc atg cct gaa gcc Arg Cys Ser Val Ala Ala Tyr Val Ser Ala Arg Thr Met Pro Glu Ala 810 815 820			2544
aag gct gat gac att gtt ggc cct gtg acg cat gaa atc ttt gag aac Lys Ala Asp Asp Ile Val Gly Pro Val Thr His Glu Ile Phe Glu Asn 825 830 835			2592
aac gtc gtc cac ttg atg tgg cag gag ccg aag gag ccc aat ggt ctg Asn Val Val His Leu Met Trp Gln Glu Pro Lys Glu Pro Asn Gly Leu 840 845 850			2640
atc gtg ctg tat gaa gtg agt tat cgg cga tat ggt gat gag gag ctg Ile Val Leu Tyr Glu Val Ser Tyr Arg Arg Tyr Gly Asp Glu Glu Leu 855 860 865			2688
cat ctc tgc gtc tcc cgc aag cac ttc gct ctg gaa cgg ggc tgc agg His Leu Cys Val Ser Arg Lys His Phe Ala Leu Glu Arg Gly Cys Arg 870 875 880 885			2736
ctg cgt ggg ctg tca ccg ggg aac tac agc gtg cga atc cgg gcc acc Leu Arg Gly Leu Ser Pro Gly Asn Tyr Ser Val Arg Ile Arg Ala Thr 890 895 900			2784
tcc ctt gcg ggc aac ggc tct tgg acg gaa ccc acc tat ttc tac gtg Ser Leu Ala Gly Asn Gly Ser Trp Thr Glu Pro Thr Tyr Phe Tyr Val 905 910 915			2832
aca gac tat tta gac gtc ccg tca aat Thr Asp Tyr Leu Asp Val Pro Ser Asn 920 925			2859
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55	60	65													
Glu	Ser	Leu	Lys	Asp	Leu	Phe	Pro	Asn	Leu	Thr	Val	Ile	Arg	Gly	Ser
70					75				80						85
Arg	Leu	Phe	Phe	Asn	Tyr	Ala	Leu	Val	Ile	Phe	Glu	Met	Val	His	Leu
					90				95						100
Lys	Glu	Leu	Gly	Leu	Tyr	Asn	Leu	Met	Asn	Ile	Thr	Arg	Gly	Ser	Val
					105				110						115
Arg	Ile	Glu	Lys	Asn	Asn	Glu	Leu	Cys	Tyr	Leu	Ala	Thr	Ile	Asp	Trp
					120				125						130
Ser	Arg	Ile	Leu	Asp	Ser	Val	Glu	Asp	Asn	His	Ile	Val	Leu	Asn	Lys
					135				140						145
Asp	Asp	Asn	Glu	Glu	Cys	Gly	Asp	Ile	Cys	Pro	Gly	Thr	Ala	Lys	Gly
					150				155						165
Lys	Thr	Asn	Cys	Pro	Ala	Thr	Val	Ile	Asn	Gly	Gln	Phe	Val	Glu	Arg
					170				175						180
Cys	Trp	Thr	His	Ser	His	Cys	Gln	Lys	Val	Cys	Pro	Thr	Ile	Cys	Lys
					185				190						195
Ser	His	Gly	Cys	Thr	Ala	Glu	Gly	Leu	Cys	Cys	His	Ser	Glu	Cys	Leu
					200				205						210
Gly	Asn	Cys	Ser	Gln	Pro	Asp	Asp	Pro	Thr	Lys	Cys	Val	Ala	Cys	Arg
					215				220						225
Asn	Phe	Tyr	Leu	Asp	Gly	Arg	Cys	Val	Glu	Thr	Cys	Pro	Pro	Pro	Tyr
					230				235						245
Tyr	His	Phe	Gln	Asp	Trp	Arg	Cys	Val	Asn	Phe	Ser	Phe	Cys	Gln	Asp
					250				255						260
Leu	His	His	Lys	Cys	Lys	Asn	Ser	Arg	Arg	Gln	Gly	Cys	His	Gln	Tyr
					265				270						275
Val	Ile	His	Asn	Asn	Lys	Cys	Ile	Pro	Glu	Cys	Pro	Ser	Gly	Tyr	Thr
					280				285						290
Met	Asn	Ser	Ser	Asn	Leu	Leu	Cys	Thr	Pro	Cys	Leu	Gly	Pro	Cys	Pro
					295				300						305
Lys	Val	Cys	His	Leu	Leu	Glu	Gly	Glu	Lys	Thr	Ile	Asp	Ser	Val	Thr
					310				315						325
Ser	Ala	Gln	Glu	Leu	Arg	Gly	Cys	Thr	Val	Ile	Asn	Gly	Ser	Leu	Ile
					330				335						340
Ile	Asn	Ile	Arg	Gly	Gly	Asn	Asn	Leu	Ala	Ala	Glu	Leu	Glu	Ala	Asn
					345				350						355
Leu	Gly	Leu	Ile	Glu	Glu	Ile	Ser	Gly	Tyr	Leu	Lys	Ile	Arg	Arg	Ser
					360				365						370
Tyr	Ala	Leu	Val	Ser	Leu	Ser	Phe	Phe	Arg	Lys	Leu	Arg	Leu	Ile	Arg
					375				380						385
Gly	Glu	Thr	Leu	Glu	Ile	Gly	Asn	Tyr	Ser	Phe	Tyr	Ala	Leu	Asp	Asn
					390				395						405
Gln	Asn	Leu	Arg	Gln	Leu	Trp	Asp	Trp	Ser	Lys	His	Asn	Leu	Thr	Thr
					410				415						420
Thr	Gln	Gly	Lys	Leu	Phe	Phe	His	Tyr	Asn	Pro	Lys	Leu	Cys	Leu	Ser
					425				430						435
Glu	Ile	His	Lys	Met	Glu	Glu	Val	Ser	Gly	Thr	Lys	Gly	Arg	Gln	Glu
					440				445						450
Arg	Asn	Asp	Ile	Ala	Leu	Lys	Thr	Asn	Gly	Asp	Lys	Ala	Ser	Cys	Glu
					455				460						465
Asn	Glu	Leu	Leu	Lys	Phe	Ser	Tyr	Ile	Arg	Thr	Ser	Phe	Asp	Lys	Ile
					470				475						485
Leu	Leu	Arg	Trp	Glu	Pro	Tyr	Trp	Pro	Pro	Asp	Phe	Arg	Asp	Leu	Leu
					490				495						500
Gly	Phe	Met	Leu	Phe	Tyr	Lys	Glu	Ala	Pro	Tyr	Gln	Asn	Val	Thr	Glu
					505				510						515
Phe	Asp	Gly	Gln	Asp	Ala	Cys	Gly	Ser	Asn	Ser	Trp	Thr	Val	Val	Asp
					520				525						530
Ile	Asp	Pro	Pro	Leu	Arg	Ser	Asn	Asp	Pro	Lys	Ser	Gln	Asn	His	Pro
					535				540						545

Gly Trp Leu Met Arg Gly Leu Lys Pro Trp Thr Gln Tyr Ala Ile Phe
 550 555 560 565
 Val Lys Thr Leu Val Thr Phe Ser Asp Glu Arg Arg Thr Tyr Gly Ala
 570 575 580
 Lys Ser Asp Ile Ile Tyr Val Gln Thr Asp Ala Thr Asn Pro Ser Val
 585 590 595
 Pro Leu Asp Pro Ile Ser Val Ser Asn Ser Ser Gln Ile Ile Leu
 600 605 610
 Lys Trp Lys Pro Pro Ser Asp Pro Asn Gly Asn Ile Thr His Tyr Leu
 615 620 625
 Val Phe Trp Glu Arg Gln Ala Glu Asp Ser Glu Leu Phe Glu Leu Asp
 630 635 640 645
 Tyr Cys Leu Lys Gly Leu Lys Leu Pro Ser Arg Thr Trp Ser Pro Pro
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 Phe Glu Ser Glu Asp Ser Gln Lys His Asn Gln Ser Glu Tyr Glu Asp
 665 670 675
 Ser Ala Gly Glu Cys Cys Ser Cys Pro Lys Thr Asp Ser Gln Ile Leu
 680 685 690
 Lys Glu Leu Glu Glu Ser Ser Phe Arg Lys Thr Phe Glu Asp Tyr Leu
 695 700 705
 His Asn Val Val Phe Val Pro Arg Lys Thr Ser Ser Gly Thr Gly Ala
 710 715 720 725
 Glu Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly
 730 735 740
 Asn Val Thr Val Ala Val Pro Thr Val Ala Ala Phe Pro Asn Thr Ser
 745 750 755
 Ser Thr Ser Val Pro Thr Ser Pro Glu Glu His Arg Pro Phe Glu Lys
 760 765 770
 Val Val Asn Lys Glu Ser Leu Val Ile Ser Gly Leu Arg His Phe Thr
 775 780 785
 Gly Tyr Arg Ile Glu Leu Gln Ala Cys Asn Gln Asp Thr Pro Glu Glu
 790 795 800 805
 Arg Cys Ser Val Ala Ala Tyr Val Ser Ala Arg Thr Met Pro Glu Ala
 810 815 820
 Lys Ala Asp Asp Ile Val Gly Pro Val Thr His Glu Ile Phe Glu Asn
 825 830 835
 Asn Val Val His Leu Met Trp Gln Glu Pro Lys Glu Pro Asn Gly Leu
 840 845 850
 Ile Val Leu Tyr Glu Val Ser Tyr Arg Arg Tyr Gly Asp Glu Glu Leu
 855 860 865
 His Leu Cys Val Ser Arg Lys His Phe Ala Leu Glu Arg Gly Cys Arg
 870 875 880 885
 Leu Arg Gly Leu Ser Pro Gly Asn Tyr Ser Val Arg Ile Arg Ala Thr
 890 895 900
 Ser Leu Ala Gly Asn Gly Ser Trp Thr Glu Pro Thr Tyr Phe Tyr Val
 905 910 915
 Thr Asp Tyr Leu Asp Val Pro Ser Asn
 920 925